Claims

What is claimed is:

1. A method of prenatal diagnosis comprising steps of:
providing a sample of amniotic fluid fetal DNA;
analyzing the amniotic fluid fetal DNA by hybridization to obtain fetal genomic information; and
based on the fetal genomic information obtained, providing a prenatal diagnosis.

2. The method of claim 1, wherein the amniotic fluid fetal DNA is obtained by:
providing a sample of amniotic fluid obtained from a woman pregnant with a fetus;
removing cell populations from the sample of amniotic fluid to obtain a remaining amniotic material; and
treating the remaining amniotic material such that cell-free fetal DNA present in the remaining material is extracted and made available for analysis, resulting in amniotic fluid fetal DNA.

3. The method of claim 2, wherein substantially all cell populations are removed from the sample of amniotic fluid and wherein the amniotic fluid fetal DNA consists essentially of cell-free fetal DNA.

4. The method of claim 2, wherein the remaining amniotic material comprises some cells and wherein the amniotic fluid fetal DNA comprises cell-free fetal DNA and DNA originating from the cells present in the remaining amniotic material.

5. The method of claim 2 further comprising steps of:
freezing the remaining amniotic material to obtain a frozen sample;
storing the frozen sample for a period of time under suitable storage conditions; and
thawing the frozen sample prior to the treating step.

6. The method of claim 5 further comprising removing substantially all cell populations that are still present in the remaining amniotic material after the thawing step and prior to the treating step.

7. The method of claim 1, wherein analyzing the amniotic fluid fetal DNA by hybridization to obtain fetal genomic information comprises using an array.

8. The method of claim 7, wherein the array is a cDNA array.

9. The method of claim 7, wherein the array is an oligonucleotide array.

10. The method of claim 7, wherein the array is a SNP array.

11. The method of claim 7, wherein analyzing the amniotic fluid fetal DNA is performed using array-based comparative genomic hybridization.

12. The method of claim 1 further comprising amplifying the amniotic fluid fetal DNA prior to the analyzing step, resulting in amplified amniotic fluid fetal DNA.

13. The method of claim 12, wherein amplifying the amniotic fluid fetal DNA comprises using PCR.

14. The method of claim 1 further comprising labeling the amniotic fluid fetal DNA with a detectable agent prior to the analyzing step, resulting in labeled amniotic fluid fetal DNA.

15. The method of claim 14, wherein the detectable agent comprises a fluorescent label.

16. The method of claim 15, wherein the fluorescent label comprises a fluorescent dye selected from the group consisting of Cy-3™, Cy-5™, Texas Red, FITC, Spectrum Red™, Spectrum Green™, phycoerythrin, a rhodamine, a fluorescein, a fluorescein isothiocyanate, a carbocyanine, a merocyanine, a styryl dye, an oxonol dye, a BODIPY dye, equivalents thereof, analogues thereof, derivatives thereof, and any combination thereof.

17. The method of claim 15, wherein the fluorescent label comprises Cy-3™ or Cy-5™.

18. The method of claim 15, wherein the fluorescent label comprises Spectrum Red™ or Spectrum Green™.

19. The method of claim 14, wherein labeling the amniotic fluid fetal DNA comprises random priming, nick translation, PCR or tailing.

20. The method of claim 14, wherein the detectable agent comprises biotin or dioxigenin.

21. The method of claim 1, wherein fetal genomic information includes chromosomal abnormalities and genome copy number changes at multiple genomic loci.

22. The method of claim 1, wherein providing a prenatal diagnosis comprises determining the sex of the fetus.

23. The method of claim 1, wherein providing a prenatal diagnosis comprises detecting and identifying a chromosomal abnormality.

24. The method of claim 1, wherein providing a prenatal diagnosis comprises identifying a disease or condition associated with a chromosomal abnormality.

25. The method of claim 2, wherein the fetus is suspected of having a chromosomal abnormality.

26. The method of claim 2, wherein the fetus is suspected of having a disease or condition associated with a chromosomal abnormality.

27. The method of claim 2, wherein the pregnant woman is 35 or more than 35 years old.

28. The method of claim 23, 24, 25 or 26, wherein the chromosomal abnormality is selected from the group consisting of an extra individual chromosome, a missing individual chromosome, an extra portion of a chromosome, a missing portion of a chromosome, a break, a ring, a chromosomal rearrangement, and any combination thereof.

29. The method of claim 23, 24, 25 or 26, wherein the chromosomal abnormality is a chromosomal rearrangement selected from the group consisting of a translocation, an inversion, a duplication, a deletion, an addition, and any combination thereof.

30. The method of claim 23, 24, 25 or 26, wherein the chromosomal abnormality is selected from the group consisting of an extra chromosome 21, a missing chromosome 21, an extra portion of chromosome 21, a missing portion of chromosome 21, a rearrangement of chromosome 21, and any combination thereof.

31. The method of claim 23, 24, 25 or 26, wherein the chromosomal abnormality is not detectable by G-banding analysis or metaphase CGH.

32. The method of claim 23, 24, 25 or 26, wherein the chromosomal abnormality is a microdeletion, a microduplication, or a subtelomeric rearrangement.

33. The method of claim 23, 24, 25 or 26, wherein the chromosomal abnormality is selected from the group consisting of an extra chromosome 13, 18, X or Y, a chromosomal aberration involving chromosome 1, a deletion of chromosome portion 1q21, a deletion of chromosome portion 4p16, a chromosomal aberration involving chromosome 4, a deletion on chromosome 5, a chromosomal aberration involving chromosome 7, a deletion of chromosome portion 7q11.23, a chromosomal aberration involving chromosome 8, a translocation involving chromosome 9 and chromosome 22, a chromosomal aberration involving chromosome 10, a chromosomal aberration involving chromosome 11, a deletion of chromosome portion 13q14, a deletion of chromosome portion 15q11-q13, a deletion of

chromosome portion 15q21.1, a deletion of chromosome portion 16p13.3, a deletion of chromosome portion 17p11.2, a deletion of chromosome portion 17p13.3, a chromosomal aberration involving chromosome19, a deletion of chromosome portion 22q11, and a chromosomal aberration involving chromosome X.

34. The method of claim 24 or 26, wherein the disease or condition associated with a chromosomal abnormality is an aneuploidy.

35. The method of claim 34, wherein the aneuploidy is selected from the group consisting of Down syndrome, Patau syndrome, Edward syndrome, Turner syndrome, Klinefelter syndrome and XYY disease.

36. The method of claim 24 or 26, wherein the disease or condition associated with a chromosomal abnormality is an X-linked disorder.

37. The method of claim 36, wherein the X-linked disorder is selected from the group consisting of Hemophilia A, Duchenne muscular dystrophy, Lesch-Nyhan syndrome, severe combined immunodeficiency, and Fragile X syndrome.

38. The method of claim 24 or 26, wherein the disease or condition is associated with a chromosomal abnormality that is not detectable by G-banding analysis or metaphase CGH.

39. The method of claim 24 or 26, wherein the disease or condition associated with a chromosomal abnormality is a microdeletion/microduplication syndrome.

40. The method of claim 39, wherein the microdeletion/microduplication syndrome is selected from the group consisting of Prader-Willi syndrome, Angelman syndrome, DiGeorge syndrome, Smith-Magenis syndrome, Rubinstein-Taybi syndrome, Miller-Dieker syndrome, Williams syndrome, and Charcot-Marie-Tooth syndrome.

41. The method of claim 24 or 26, wherein the disease or condition is associated with a subtelomeric rearrangement.

42. The method of claim 24 or 26, wherein the disease or condition associated with a chromosomal abnormality is selected from the group consisting of Cri du Chat syndrome, Retinoblastoma, Wolf-Hirschhorn syndrome, Wilms tumor, spinobulbar muscular atrophy, cystic fibrosis, Gaucher disease, Marfan syndrome, and sickle cell anemia.

43. A method of prenatal diagnosis performed by analyzing amniotic fluid fetal DNA by array-based comparative genomic hybridization, the method comprising steps of:

providing a test sample of amniotic fluid fetal DNA, wherein the test sample comprises a plurality of nucleic acid segments comprising a substantially complete first genome with an unknown karyotype and labeled with a first detectable agent;

providing a reference sample, wherein the reference sample comprises a plurality of nucleic acid segments comprising a substantially complete second genome with a known karyotype and labeled with a second detectable agent;

providing an array comprising a plurality of genetic probes, wherein each genetic probe is immobilized to a discrete spot on a substrate surface to form the array and wherein together the genetic probes comprise a substantially complete third genome or a subset of a third genome;

contacting the array simultaneously with the test and reference samples under conditions wherein the nucleic acid segments in the samples can specifically hybridize to the genetic probes on the array;

determining the binding of the individual nucleic acids of the test sample and reference sample to the individual genetic probes immobilized on the array to obtain a relative binding pattern; and

based on the relative binding pattern obtained, providing a prenatal diagnosis.

44. The method of claim 43, wherein the nucleic acids of the test sample and reference sample are labeled by random priming, nick translation, PCR or tailing.

45. The method of claim 43, wherein the first detectable agent comprises a first fluorescent label and the second detectable agent comprises a second fluorescent label.

46. The method of claim 43, wherein the first fluorescent label and second fluorescent label produce a dual-color fluorescence upon excitation.

47. The method of claim 46, wherein the first fluorescent label comprises Cy-3™ and the second fluorescent label comprises Cy-5™.

48. The method of claim 46, wherein the first fluorescent label comprises Cy-5™ and the second fluorescent label comprises Cy-3™.

49. The method of claim 46, wherein the first fluorescent label comprises Spectrum Red™ and the second fluorescent label comprises Spectrum Green™.

50. The method of claim 46, wherein the first fluorescent label comprises Spectrum Green™ and the second fluorescent label comprises Spectrum Red™.

51. The method of claim 43, wherein the hybridization capacity of high copy number repeat sequences present in the nucleic acid segments of the test sample and reference sample is suppressed.

52 The method of claim 51, wherein the hybridization capacity of high copy number repeat sequences is suppressed by adding unlabeled blocking nucleic acids to the test sample and reference sample prior to the contacting step.

53. The method of claim 52, wherein the unlabeled blocking nucleic acids are Human Cot-1 DNA.

54. The method of claim 43, wherein the amniotic fluid fetal DNA is obtained by:

providing a sample of amniotic fluid obtained from a woman pregnant with a fetus;

removing cell populations from the sample of amniotic fluid to obtain a remaining amniotic material; and

treating the remaining amniotic material such that cell-free fetal DNA present in the remaining material is extracted and made available for analysis, resulting in amniotic fluid fetal DNA.

55. The method of claim 54, wherein substantially all cell populations are removed from the sample of amniotic fluid and wherein the amniotic fluid fetal DNA consists essentially of cell-free fetal DNA.

56. The method of claim 54, wherein the remaining amniotic material comprises some cells and wherein the amniotic fluid fetal DNA comprises cell-free fetal DNA and DNA originating from the cells present in the remaining amniotic material.

57. The method of claim 54 further comprising steps of:

freezing the remaining amniotic material to obtain a frozen sample;

storing the frozen sample for a period of time under suitable storage conditions; and

thawing the frozen sample prior to the treating step.

58. The method of claim 54 further comprising amplifying the amniotic fluid fetal DNA using PCR, resulting in amplified amniotic fluid fetal DNA.

59. The method of claim 54 further comprising labeling the amniotic fluid fetal DNA with a detectable agent by random priming, nick translation, PCR or tailing, resulting in labeled amniotic fluid fetal DNA.

60. The method of claim 43, wherein the karyotype of the second genome has been determined by G-banding analysis, metaphase CGH, FISH or SKY.

61. The method of claim 43, wherein determining the binding of the individual nucleic acids of the test and reference samples to the individual genetic probes immobilized on the array to obtain a relative binding pattern comprises steps of:

measuring the intensity of the signals produced by the first detectable agent and second detectable agent at each discrete spot on the array; and

determining the ratio of the intensities of the signals for each spot of the array.

62. The method of claim 43, wherein determining the binding of the individual nucleic acids of the test and reference samples to the individual genetic probes immobilized on the array to obtain a relative binding pattern comprises steps of:

using a computer-assisted imaging system capable of acquiring multicolor fluorescence images to obtain a fluorescence image of the array after hybridization; and

using a computer-assisted image analysis system to analyze the fluorescence image obtained, to interpret data imaged from the array and to display results as genome copy number ratios as a function of genomic locus in the third genome.

63. The method of claim 43, wherein providing a prenatal diagnosis comprises determining the sex of the fetus carried by the pregnant woman.

64. The method of claim 43, wherein providing a prenatal diagnosis comprises detecting and identifying a chromosomal abnormality.

65. The method of claim 43, wherein providing a prenatal diagnosis comprises identifying a disease or condition associated with a chromosomal abnormality.

66. The method of claim 43, wherein the amniotic fluid fetal DNA originates from a fetus suspected of having a chromosomal abnormality.

67. The method of claim 43, wherein the amniotic fluid fetal DNA originates from a fetus suspected of having a disease or condition associated with a chromosomal abnormality.

68. The method of claim 43, wherein the amniotic fluid fetal DNA has been extracted from a sample of amniotic fluid obtained from a pregnant woman who is 35 or more than 35 years old.

69. The method of claim 64, 65, 66 or 67, wherein the chromosomal abnormality is selected from the group consisting of an extra individual chromosome, a missing individual chromosome, an extra portion of a chromosome, a missing portion of a chromosome, a break, a ring, a chromosomal rearrangement, and any combination thereof.

70. The method of claim 64, 65, 66 or 67, wherein the chromosomal abnormality is a chromosomal rearrangement selected from the group consisting of a translocation, an inversion, a duplication, a deletion, an addition, and any combination thereof.

71. The method of claim 64, 65, 66 or 67, wherein the chromosomal abnormality is selected from the group consisting of an extra chromosome 21, a missing chromosome 21, an extra portion of chromosome 21, a missing portion of chromosome 21, a rearrangement of chromosome 21, and any combination thereof.

72. The method of claim 64, 65, 66 or 67, wherein the chromosomal abnormality is not detectable by G-banding analysis or metaphase CGH.

73. The method of claim 64, 65, 66 or 67, wherein the chromosomal abnormality is a microdeletion, a microduplication or a subtelomeric rearrangement.

74. The method of claim 64, 65, 66 or 67, wherein the chromosomal abnormality is selected from the group consisting of an extra chromosome 13, 18, X or Y, a chromosomal aberration involving chromosome 1, a deletion of chromosome portion 1q21, a deletion of chromosome portion 4p16, a

chromosomal aberration involving chromosome 4, a deletion on chromosome 5, a chromosomal aberration involving chromosome 7, a deletion of chromosome portion 7q11.23, a chromosomal aberration involving chromosome 8, a translocation involving chromosome 9 and chromosome 22, a chromosomal aberration involving chromosome 10, a chromosomal aberration involving chromosome 11, a deletion of chromosome portion 13q14, a deletion of chromosome portion 15q11-q13, a deletion of chromosome portion 15q21.1, a deletion of chromosome portion 16p13.3, a deletion of chromosome portion 17p11.2, a deletion of chromosome portion 17p13.3, a chromosomal aberration involving chromosome 19, a deletion of chromosome portion 22q11, and a chromosomal aberration involving chromosome X.

75. The method of claim 65 or 67, wherein the disease or condition associated with a chromosomal abnormality is an aneuploidy.

76. The method of claim 75, wherein the aneuploidy is selected from the group consisting of Down syndrome, Patau syndrome, Edward syndrome, Turner syndrome, Klinefelter syndrome and XYY disease.

77. The method of claim 65 or 67, wherein the disease or condition associated with a chromosomal abnormality is an X-linked disorder.

78. The method of claim 77, wherein the X-linked disorder is selected from the group consisting of Hemophilia A, Duchenne muscular dystrophy, Lesch-Nyhan syndrome, severe combined immunodeficiency, and Fragile X syndrome.

79. The method of claim 65 or 67, wherein the disease or condition is associated with a chromosomal abnormality that is not detectable by G-banding analysis or metaphase CGH.

80. The method of claim 65 or 67, wherein the disease or condition associated with a chromosomal abnormality is a microdeletion/microduplication syndrome.

81. The method of claim 80, wherein the microdeletion/microduplication syndrome is selected from the group consisting of Prader-Willi syndrome, Angelman syndrome, DiGeorge syndrome, Smith-Magenis syndrome, Rubinstein-Taybi syndrome, Miller-Dieker syndrome, Williams syndrome, and Charcot-Marie-Tooth syndrome.

82. The method of claim 65 or 67, wherein the disease or condition is associated with a subtelomeric rearrangement.

83. The method of claim 65 or 67, wherein the disease or condition associated with a chromosomal abnormality is selected from the group consisting of Cri du Chat syndrome, Retinoblastoma, Wolf-Hirschhorn syndrome, Wilms tumor, spinobulbar muscular atrophy, cystic fibrosis, Gaucher disease, Marfan syndrome, and sickle cell anemia.

84. A method of testing amniotic fluid fetal DNA by array-based comparative genomic hybridization comprising steps of:

providing a test sample of amniotic fluid fetal DNA, wherein the test sample comprises a plurality of nucleic acid segments comprising a substantially complete first genome with a chromosomal micro-abnormality and labeled with a first detectable agent;

providing a reference sample of control genomic DNA, wherein the reference sample comprises a plurality of nucleic acid segments comprising a substantially complete second genome with a known karyotype and labeled with a second detectable agent;

providing an array comprising a plurality of genetic probes, wherein each genetic probe is immobilized to a discrete spot on a substrate surface to form the array and wherein together the genetic probes comprise a substantially complete third genome or a subset of a third genome;

contacting the array simultaneously with the test sample and reference sample under conditions wherein the nucleic acid segments of the test and reference samples can specifically hybridize to the genetic probes immobilized on the array;

using a computer-assisted imaging system capable of acquiring multicolor fluorescence images to obtain a fluorescence image of the array after hybridization;

using a computer-assisted image analysis system to analyze the fluorescence image obtained, to interpret data imaged from the array and to display results as genome copy number ratios as a function of genomic locus in the third genome;

determining the karyotype of the first genome by FISH analysis; and

comparing the results displayed as genome copy number ratios to the karyotype of the first genome determined by FISH.

85. The method of claim 84, wherein comparing the results displayed as genome copy number ratios to the karyotype of the first genome determined by FISH comprises evaluating the degree of consistency between the results displayed and the karyotype of the first genome determined by FISH.

86. The method of claim 84, wherein comparing the results displayed as genome copy number ratios to the karyotype of the first genome determined by FISH comprises comparing the sensitivity of detection of the chromosomal micro-abnormality present in the first genome by FISH and by array-based comparative genomic hybridization.

87. The method of claim 84, wherein comparing the results displayed as genome copy number ratios to the karyotype of the first genome determined by FISH comprises comparing the selectivity of detection of the chromosomal micro-abnormality present in the first genome by FISH and by array-based comparative genomic hybridization.

88. The method of claim 84, wherein the chromosomal micro-abnormality is a microdeletion, a microduplication or a subtelomeric rearrangement.

89. The method of claim 84, wherein the chromosomal micro-abnormality is selected from the group consisting of a deletion of chromosome portion 1q22, a deletion of chromosome portion 7q11.23, a deletion of chromosome portion 8q21, a deletion of chromosome portion 10q21.1-q22.1, a deletion of chromosome portion 15q11-q13, a deletion of chromosome portion 16p13.3, a deletion of chromosome portion 17p11.2, a deletion of chromosome portion 17p13.3, a deletion of chromosome portion 19q13.1-q13.2, and a deletion of chromosome portion 22q11.2.

90. The method of claim 84, wherein the nucleic acids of the test sample and reference sample are labeled by random priming, nick translation, PCR or tailing.

91. The method of claim 84, wherein the first detectable agent comprises a first fluorescent label, the second detectable agent comprises a second fluorescent label, and the first and second fluorescent labels produce a dual-color fluorescence upon excitation.

92. The method of claim 91, wherein the first fluorescent label comprises Cy-3™ and the second fluorescent label comprises Cy-5™.

93. The method of claim 91, wherein the first fluorescent label comprises Cy-5™ and the second fluorescent label comprises Cy-3™.

94. The method of claim 91, wherein the first fluorescent label comprises Spectrum Red™ and the second fluorescent label comprises Spectrum Green™.

95. The method of claim 91, wherein the first fluorescent label comprises Spectrum Green™ and the second fluorescent label comprises Spectrum Red™

96. The method of claim 84, wherein the hybridization capacity of high copy number repeat sequences present in the nucleic acid segments of the test sample and reference sample is suppressed by adding Human Cot-1 DNA to the test and reference samples before the contacting step.

97. The method of claim 84, wherein the amniotic fluid fetal DNA is obtained by:

providing a sample of amniotic fluid obtained from a woman pregnant with a fetus;

removing cell populations from the sample of amniotic fluid to obtain a remaining amniotic material; and

treating the remaining amniotic material such that cell-free fetal DNA present in the remaining material is extracted and made available for analysis, resulting in amniotic fluid fetal DNA.

98. The method of claim 97, wherein substantially all cell populations are removed from the sample of amniotic fluid and wherein the amniotic fluid fetal DNA consists essentially of cell-free fetal DNA.

99. The method of claim 97, wherein the remaining amniotic material comprises some cells and wherein the amniotic fluid fetal DNA comprises cell-free fetal DNA and DNA originating from the cells present in the remaining amniotic material.

100. The method of claim 97 further comprising steps of:

freezing the remaining amniotic material to obtain a frozen sample;

storing the frozen sample for a period of time under suitable storage conditions; and

thawing the frozen sample prior to the treating step.

101. The method of claim 97 further comprising amplifying the amniotic fluid fetal DNA using PCR, resulting in amplified amniotic fluid fetal DNA.

102. The method of claim 97 further comprising labeling the amniotic fluid fetal DNA with a detectable agent by random priming, nick translation, PCR or tailing, resulting in labeled extracted amniotic fluid fetal DNA.

103. The method of claim 84, wherein the karyotype of the second genome has been determined by G-banding analysis, metaphase CGH, FISH or SKY.

104. A method for identifying a chromosomal abnormality by analyzing amniotic fluid fetal DNA by array-based comparative genomic hybridization, the method comprising steps of:

providing a test sample of amniotic fluid fetal DNA, wherein the amniotic fluid fetal DNA originates from a fetus determined to have multiple congenital anomalies by sonographic examination, and wherein the test sample comprises a plurality of nucleic acid segments comprising a substantially complete first genome with a normal karyotype and labeled with a first detectable agent;

providing a reference sample of control amniotic fluid fetal DNA, wherein the control amniotic fluid fetal DNA originates from a fetus determined to have no congenital anomalies by sonographic examination, and wherein the reference sample comprises a plurality of nucleic acid segments comprising a substantially complete second genome with a normal karyotype and labeled with a second detectable agent;

providing an array comprising a plurality of genetic probes, wherein each genetic probe is immobilized to a discrete spot on a substrate surface to form the array and wherein together the genetic probes comprise a substantially complete third genome or a subset of a third genome;

contacting the array simultaneously with the test sample and reference sample under conditions wherein the nucleic acid segments in the samples can specifically hybridize to the genetic probes immobilized on the array;

using a computer-assisted imaging system capable of acquiring multicolor fluorescence images to obtain a fluorescence image of the array after hybridization;

using a computer-assisted image analysis system to analyze the fluorescence image obtained, to interpret data imaged from the array and to display results as genome copy number ratios as a function of genomic locus in the third genome; and

analyzing the results displayed to detect and identify any chromosomal abnormality present.

105. The method of claim 104, wherein the karyotype of the test sample has been determined by metaphase CGH analysis with a 550 band level of resolution.

106. The method of claim 104, wherein the chromosomal abnormality present in the first genome is a chromosomal micro-abnormality that is not detectable by metaphase CGH analysis with a 550 band level of resolution.

107. The method of claim 106, wherein the chromosomal micro-abnormality is selected from the group consisting of a micro-addition, a micro-deletion, a micro-duplication, a micro-inversion, a micro-translocation, a subtelomeric rearrangement and any combination thereof.

108. The method of claim 104, wherein the nucleic acids of the test sample and reference sample are labeled by random priming, nick translation, PCR or tailing.

109. The method of claim 104, wherein the first detectable agent comprises a first fluorescent label, the second detectable agent comprises a second fluorescent label, and the first and second fluorescent labels produce a dual-color fluorescence upon excitation.

110. The method of claim 109, wherein the first fluorescent label comprises Cy-3™ and the second fluorescent label comprises Cy-5™.

111. The method of claim 109, wherein the first fluorescent label comprises Cy-5™ and the second fluorescent label comprises Cy-3™.

112. The method of claim 109, wherein the first fluorescent label comprises Spectrum Red™ and the second fluorescent label comprises Spectrum Green™.

113. The method of claim 109, wherein the first fluorescent label comprises Spectrum Green™ and the second fluorescent label comprises Spectrum Red™.

114. The method of claim 104, wherein the hybridization capacity of high copy number repeat sequences present in the nucleic acid segments of the test sample and reference sample is suppressed by adding Human Cot-1 DNA to the test and reference samples before the contacting step.

115. The method of claim 104, wherein the amniotic fluid fetal DNA from the test sample is obtained by:

providing a sample of amniotic fluid obtained from a woman pregnant with a fetus;

removing cell populations from the sample of amniotic fluid to obtain a remaining amniotic material; and

treating the remaining amniotic material such that cell-free fetal DNA present in the remaining material is extracted and made available for analysis, resulting in amniotic fluid fetal DNA.

116. The method of claim 115, wherein substantially all cell populations are removed from the sample of amniotic fluid and the amniotic fluid fetal DNA consists essentially of cell-free fetal DNA.

117. The method of claim 115, wherein the remaining amniotic material comprises some cells and the amniotic fluid fetal DNA comprises cell-free fetal DNA and DNA originating from the cells present in the remaining amniotic material.

118. The method of claim 104, wherein the control amniotic fluid fetal DNA from the reference sample is obtained by:

providing a sample of amniotic fluid obtained from a woman pregnant with a fetus;

removing cell populations from the sample of amniotic fluid to obtain a remaining amniotic material; and

treating the remaining amniotic material such that cell-free fetal DNA present in the remaining material is extracted and made available for analysis, resulting in control amniotic fluid fetal DNA.

119. The method of claim 118, wherein substantially all cell populations are removed from the sample of amniotic fluid and the control amniotic fluid fetal DNA consists essentially of cell-free fetal DNA.

120. The method of claim 118, wherein the remaining amniotic material comprises some cells and the control amniotic fluid fetal DNA comprises cell-free fetal DNA and DNA originating from the cells present in the remaining amniotic material.

121. The method of claim 115 or 118 further comprising steps of:

freezing the remaining amniotic material to obtain a frozen sample;

storing the frozen sample for a period of time under suitable storage conditions; and

thawing the frozen sample prior to the treating step.

122. The method of claim 115 further comprising amplifying the amniotic fluid fetal DNA using PCR, resulting in amplified amniotic fluid fetal DNA.

123. The method of claim 118 further comprising amplifying the control amniotic fluid fetal DNA using PCR, resulting in amplified control amniotic fluid fetal DNA

124. The method of claim 115 further comprising labeling the amniotic fluid fetal DNA with a detectable agent by random priming, nick translation, PCR or tailing, resulting in labeled amniotic fluid fetal DNA.

125. The method of claim 118 further comprising labeling the control amniotic fluid fetal DNA with a detectable agent by random priming, nick translation, PCR or tailing, resulting in labeled control amniotic fluid fetal DNA.

126. The method of claim 104, wherein the karyotype of the second genome has been determined by G-banding analysis, metaphase CGH, FISH or SKY.

127. The method of claim 104, wherein the test and reference samples are matched for fetal gender, site of sample acquisition, gestational age, and storage time.

128. A kit comprising the following components:

materials to extract cell-free fetal DNA from a sample of amniotic fluid obtained from a pregnant woman;

an array comprising a plurality of genetic probes, wherein each genetic probe is immobilized to a discrete spot on a substrate surface to form the array and wherein together the genetic probes comprise a substantially complete genome or a subset of a genome; and

instructions for using the array as set forth in claim 43, 84 or 104.

129. The kit of claim 128 further comprising materials to label a first sample of DNA with a first detectable agent and a second sample of DNA with a second detectable agent.

130. The kit of claim 129, wherein the first detectable agent comprises a first fluorescent label, the second detectable agent comprises a second fluorescent label, and the first and second fluorescent labels produce a dual-color fluorescence upon excitation.

131. The kit of claim 130 further comprising materials to label a first sample of DNA and a second sample of DNA with Cy-3™ and Cy-5™.

132. The kit of claim 130 further comprising materials to label a first sample of DNA and a second sample of DNA with Spectrum Red™ and Spectrum Green™.

133. The kit of claim 128 further comprising a sample of control genomic DNA with a normal, female karyotype.

134. The kit of claim 128 further comprising a sample of control genomic DNA with a normal, male karyotype.

135. The kit of claim 128 further comprising a sample of control genomic DNA with a karyotype comprising a chromosomal abnormality.

136. The kit of claim 128 further comprising hybridization and wash buffers.

137. The kit of claim 128 further comprising Human Cot-1 DNA.